

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/521,305
Source: PCT/10
Date Processed by STIC: 1/28/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

| <u>ERROR DETECTED</u> | <u>SUGGESTED CORRECTION</u> | <u>SERIAL NUMBER:</u> <u>10/521,305</u> |
|---|---|---|
| ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE | | |
| 1 <input checked="" type="checkbox"/> Wrapped Nucleic Wrapped Aminos | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping." | |
| 2 <input type="checkbox"/> Invalid Line Length | The rules require that a line not exceed 72 characters in length. This includes white spaces. | |
| 3 <input type="checkbox"/> Misaligned Amino Numbering | The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead. | |
| 4 <input type="checkbox"/> Non-ASCII | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. | |
| 5 <input type="checkbox"/> Variable Length | Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. | |
| 6 <input type="checkbox"/> PatentIn 2.0 "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. | |
| 7 <input type="checkbox"/> Skipped Sequences (OLD RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped | |
| | Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. | |
| 8 <input type="checkbox"/> Skipped Sequences (NEW RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000 | |
| 9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. | |
| 10 <input type="checkbox"/> Invalid <213> Response | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence | |
| 11 <input type="checkbox"/> Use of <220> | Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) | |
| 12 <input type="checkbox"/> PatentIn 2.0 "bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. | |
| 13 <input type="checkbox"/> Misuse of n/Xaa | "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid | |



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/521,305

DATE: 01/28/2005
TIME: 11:15:55

Input Set : A:\pto.yf.TXT
Output Set: N:\CRF4\01282005\J521305.raw

3 <110> APPLICANT: Canon Kabushiki Kaisha
 5 <120> TITLE OF INVENTION: PROBE CARRIER AND METHOD OF PRODUCING SAME
 7 <130> FILE REFERENCE: CFO17416WO
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/521,305
 C--> 9 <141> CURRENT FILING DATE: 2005-01-14
 9 <150> PRIOR APPLICATION NUMBER: JP 2002-211147
 10 <151> PRIOR FILING DATE: 2002-07-19
 12 <150> PRIOR APPLICATION NUMBER: JP 2003-197920
 13 <151> PRIOR FILING DATE: 2003-07-16
 15 <160> NUMBER OF SEQ ID NOS: 3
 17 <170> SOFTWARE: PatentIn version 3.1

**Dose Not Comply
 Corrected Diskette Needed**

ERRORED SEQUENCES

19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 18
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Artificial
 24 <220> FEATURE:
 25 <223> OTHER INFORMATION: probe
 27 <400> SEQUENCE: 1
 E--> 28 actggccgtc gtttaca
 29 18
 32 <210> SEQ ID NO: 2
 33 <211> LENGTH: 18
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Artificial
 37 <220> FEATURE:
 38 <223> OTHER INFORMATION: probe
 40 <400> SEQUENCE: 2
 E--> 41 actggccctc gtttaca
 42 18
 45 <210> SEQ ID NO: 3
 46 <211> LENGTH: 18
 47 <212> TYPE: DNA
 48 <213> ORGANISM: Artificial
 50 <220> FEATURE:
 51 <223> OTHER INFORMATION: probe
 53 <400> SEQUENCE: 3
 E--> 54 actggccgtc gtttaca
 55 18

18 (see item 1 on Error Summary Sheet)

same error

same

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/521,305

DATE: 01/28/2005
TIME: 11:15:56

Input Set : A:\pto.yf.TXT
Output Set: N:\CRF4\01282005\J521305.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/521,305

DATE: 01/28/2005
TIME: 11:15:56

Input Set : A:\pto.yf.TXT
Output Set: N:\CRF4\01282005\J521305.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:28 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:1
L:41 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:2
L:54 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:3